

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:24:23 ; Search time 18.4571 Seconds
(without alignments)
98.997 Million cell updates/sec

Title: US-09-905-691-2

Perfect score: 19
Sequence: 1 ARAARRAARARARAE 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_76.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	9	47.4	105	2 D86976	probable integrati
2	9	47.4	190	2 B70899	probable mihf prot
3	8	42.1	144	2 H72702	hypothetical prote
4	8	42.1	328	2 H83363	pyoverdine biosynt
5	8	42.1	336	2 T50935	isomerase/decarbox
6	8	42.1	356	2 A21198	H-2 class I histoc
7	8	42.1	383	2 F83490	probable multidrug
8	8	42.1	710	2 AD3479	ATP-dependent heli
9	8	42.1	897	2 T02808	conserved hypothet
10	8	42.1	998	2 T35745	probable ATP-bind
11	7	36.8	69	2 AD2110	hypothetical prote
12	7	36.8	71	2 AI3052	hypothetical prote
13	7	36.8	77	2 AH0925	hypothetical prote
14	7	36.8	110	2 T30752	hypothetical prote
15	7	36.8	145	2 E75622	hypothetical prote
16	7	36.8	157	2 D70777	hypothetical prote
17	7	36.8	179	2 C83305	transcription regu
18	7	36.8	194	2 H72638	hypothetical prote
19	7	36.8	231	2 F75459	high-affinity bran
20	7	36.8	252	2 AH3618	hypothetical prote
21	7	36.8	263	1 C39741	hypothetical 29K p
22	7	36.8	292	2 JE0233	trypsin-I - scall
23	7	36.8	315	2 G87464	nitrogen regulatio
24	7	36.8	326	2 B87557	hypothetical prote
25	7	36.8	326	2 S27534	hypothetical prote
26	7	36.8	336	2 E84295	hypothetical prote
27	7	36.8	338	2 D95851	probable oxidoredu
28	7	36.8	354	2 B55733	G protein-coupled
29	7	36.8	358	2 F87364	HlyD family secret

30 7 36.8 376 2 T35868 probable dipeptida
31 7 36.8 383 2 T35773 succinyl-CoA synth
32 7 36.8 395 1 KISMG galactokinase (EC
33 7 36.8 408 2 A87649 hypothetical prote
34 7 36.8 409 1 S72892 probable hexosyltr
35 7 36.8 411 2 H82998 probable 3-hydroxy
36 7 36.8 428 2 H87214 probable glycosyl
37 7 36.8 438 2 T36953 conserved hypothet
38 7 36.8 444 2 S35783 glycoprotein gx -
39 7 36.8 454 2 AI3467 glycine betaine/l-
40 7 36.8 474 1 BVBRCB cyAE protein - Bor
41 7 36.8 480 1 A70744 probable hexosyltr
42 7 36.8 488 2 T32754 hypothetical prote
43 7 36.8 501 2 A87474 enoyl-CoA hydratase
44 7 36.8 511 2 B87258 hypothetical prote
45 7 36.8 525 2 A72586 hypothetical prote

ALIGNMENTS

RESULT 1

D86976

Probable integration host factor [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: D86976

R:Coile, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holrc
eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: D86976

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <SFO>

A:Cross-references: GB:AL450380; NID:gl3092744; PIDN:CAC30048.1; GSPDB:GN00147

C:Genetics:

A:Gene: mihf

Query Match 47.4%; Score 9; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 10 AAARRARAE 18

Db 19 AAARRARAE 27

RESULT 2

B70899

Probable mihf protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: B70899

R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: B70899

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-190 <COL>

A:Cross-references: GB:Z80108; GB:AL123456; NID:93256012; PIDN:CAB02193.1; PID:g15428

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: mihf

C:Superfamily: Mycobacterium tuberculosis probable mihf protein

Query Match 47.4%; Score 9; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AAARRARAE 18
 DB 104 AAARRARAE 112
 |||||

RESULT 3
 H72702
 Hypothetical protein APE1039 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: H72702
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hakawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawana, H.; 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: H72702
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-144 <RAW>
 A:Cross-references: DDBJ:AF000060; NID:G5104188; PIDN:BAAR0024.1; PID:G51043810; PID:G51043810
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1039

Query Match 42.1%; Score 8; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AARRAARA 10
 DB 3 AARRAARA 10
 |||||

RESULT 4
 H83363
 pyoverdine biosynthesis protein PvCA PA2254 [imported] - Pseudomonas aeruginosa (strain ATCC 27893)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83363
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brodeur, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: H83363
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-328 <STO>
 A:Cross-references: GB:AE004651; GB:AE004091; NID:G9948277; PIDN:AAG05642.1; GSPDB:GN0010984043
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: pvCA; PA2254

Query Match 42.1%; Score 8; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAARRAA 8
 DB 319 ARAARRAA 326
 |||||

RESULT 5
 T50935
 isomerase/decarboxylase homolog Dith [imported] - Pseudomonas abietaniphila
 C:Species: Pseudomonas abietaniphila

Query Match 47.4%; Score 9; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AAARRARAE 18
 DB 104 AAARRARAE 112
 |||||

RESULT 3
 H72702
 Hypothetical protein APE1039 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: H72702
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hakawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawana, H.; 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: H72702
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-144 <RAW>
 A:Cross-references: DDBJ:AF000060; NID:G5104188; PIDN:BAAR0024.1; PID:G51043810; PID:G51043810
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1039

Query Match 42.1%; Score 8; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AARRAARA 10
 DB 3 AARRAARA 10
 |||||

RESULT 4
 H83363
 pyoverdine biosynthesis protein PvCA PA2254 [imported] - Pseudomonas aeruginosa (strain ATCC 27893)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83363
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brodeur, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: H83363
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-328 <STO>
 A:Cross-references: GB:AE004651; GB:AE004091; NID:G9948277; PIDN:AAG05642.1; GSPDB:GN0010984043
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: pvCA; PA2254

Query Match 42.1%; Score 8; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAARRAA 8
 DB 319 ARAARRAA 326
 |||||

RESULT 5
 T50935
 isomerase/decarboxylase homolog Dith [imported] - Pseudomonas abietaniphila
 C:Species: Pseudomonas abietaniphila

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
 C:Accession: T50935
 R:Martin, V.J.; Mohr, W.W.
 J. Bacteriol. 181, 2675-2682, 1999
 A:Title: A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degradant strain T50935
 A:Reference number: Z25281; MUID:99235742; PMID:10217753
 A:Accession: T50935
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-336 <MAR>
 A:Cross-references: EMBL:AF119621; PIDN:AAO21070.1
 A:Experimental source: strain BME-9; ATCC700689
 C:Genetics:
 A:Gene: dth

Query Match 42.1%; Score 8; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AAARRARA 17
 DB 105 AAARRARA 112
 |||||

RESULT 6
 A21198
 H-2 class I histocompatibility antigen pH-2D-24 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Jul-1990 #sequence_revision 31-Jul-1992 #text_change 23-Jul-1999
 C:Accession: A21198
 R:Lalanne, J.L.; Cochet, M.; Kummer, A.M.; Gachelin, G.; Kourilsky, P.
 Proc. Natl. Acad. Sci. U.S.A. 80, 7561-7565, 1983
 A:Title: Different exon-intron organization at the 5' part of a mouse class I gene is associated with a different pattern of polymorphism
 A:Reference number: A21198; MUID:84170268; PMID:6143316
 A:Accession: A21198
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-356 <LAL>
 A:Cross-references: GB:K01182; NID:G199544; PIDN:AAA39653.1; PID:G387468
 A:Note: the authors translated the codon CCC for residue 288 as Ser
 C:Superfamily: Class I histocompatibility antigen; immunoglobulin homology
 F:205-270/Domain: immunoglobulin homology <IM>

Query Match 42.1%; Score 8; DB 2; Length 356;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RAARAAR 13
 DB 20 RAARAAR 27
 |||||

RESULT 7
 F83490
 Probable multidrug resistance efflux pump PA1237 [imported] - Pseudomonas aeruginosa
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: F83490
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brodeur, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: F83490
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-383 <STO>
 A:Cross-references: GB:AE004553; GB:AE004091; NID:G9947164; PIDN:AAG04626.1; GSPDB:GN0010984043
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1237
 C:Superfamily: multidrug resistance protein A; lipoyl/biotin-binding homology

Query Match 42.1%; Score 8; DB 2; Length 383;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ARAAARRA 15
 Db 187 ARAAARRA 194
 |||||

RESULT 8
 AD3479
 ATP-dependent helicase hrbp BMEI1818 [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 14-Apr-2003
 C:Accession: AD3479
 R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:1175668
 A:Accession: AD3479
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-710 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL52999.1; PID:g17983853; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI1818
 A:Map position: 1
 C:Superfamily: HrpB type ATP-dependent RNA helicase

Query Match 42.1%; Score 8; DB 2; Length 710;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAAARR 14
 Db 156 ARAAARR 163
 |||||

RESULT 9
 T02808
 conserved hypothetical protein YPL199c, L2602.6 [imported] - Leishmania major (strain F
 C:Species: Leishmania major
 C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
 C:Accession: D81457; T02808
 R:Wyller, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
 Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
 A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
 A:Reference number: A81455; MUID:99178987; PMID:10077609
 A:Accession: D81457
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-897 <PYL>
 A:Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24631.1; PID:g2995584; GSPDB:GN00
 A:Experimental source: strain MHOM/IL/81/Friedlin
 C:Genetics:
 A:Gene: L2602.6
 A:Map position: 1

Query Match 42.1%; Score 8; DB 2; Length 897;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AAARRARA 17
 Db 326 AAARRARA 333
 |||||

RESULT 10
 T33745
 probable ATP-binding RNA helicase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor
 C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C:Accession: T33745
 R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
 submitted to the EMBL Data Library, August 1999
 A:Reference number: Z21588
 A:Accession: T33745
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-998 <SAD>
 A:Cross-references: EMBL:AL109732; PIDN:CAB52056.1; GSPDB:GN00070; SCOEDB:SC7H2.14
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC7H2.14

Query Match 42.1%; Score 8; DB 2; Length 998;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAAARR 14
 Db 70 ARAAARR 77
 |||||

RESULT 11
 AD2110
 hypothetical protein asl2435 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AD2110
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AD2110
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-69 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA074134.1; PID:g17131527; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: asl2435

Query Match 36.8%; Score 7; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AAARRAR 16
 Db 54 AAARRAR 60
 |||||

RESULT 12
 AI3052
 hypothetical protein Atu4038 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AI3052
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; MCL
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AI3052
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-71 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AAL44839.1; PID:g17742483; GSPDB:GN00187

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu4038

A:Map position: linear chromosome

Query Match 36.8%; Score 7; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAARRAA 8

DB 39 RAARRAA 45

RESULT 13

AH0925

hypothetical protein STX3665 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AH0925

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, M.; Mouton, S.; O'Garra, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; White, N.; Farrar, M.; Mouton, S.; O'Garra, P.

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AH0925

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD09426.1; PID:g16504543; GSPDB:GN00176

C:Genetics:

A:Gene: STX3665

Query Match

Best Local Similarity 36.8%; Score 7; DB 2; Length 77;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 RRARAA 19

DB 30 RRARAA 36

RESULT 14

T30752

hypothetical protein 150R - Molluscum contagiosum virus 1

N:Alternate names: MC150R

C:Species: Molluscum contagiosum virus 1

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000

C:Accession: T30752

R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.

Science 273, 813-816, 1996

A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host range

A:Reference number: 220876; MUID:96325459; PMID:8670425

A:Accession: T30752

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-110 <SEN>

A:Cross-references: EMBL:U60315; MUID:g1491943; PIDN:AAC55278.1; PID:g1492093

C:Genetics:

A:Note: MC150R

C:Superfamily: Molluscum contagiosum virus 1 hypothetical protein 150R

Query Match

Best Local Similarity 36.8%; Score 7; DB 2; Length 110;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AAARRAR 16

DB 91 AAARRAR 97

RESULT 15

E75622

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: E75622

R:White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: E75622

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-145 <WHL>

A:Cross-references: GB:AB001826; NID:96460827; PIDN:AAF12646.1; PID:g6460942; TIGR:DR

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRB0040

A:Map position: megaplasmid

A:Genome: plasmid

A:Note: plasmid MFI

Query Match 36.8%; Score 7; DB 2; Length 145;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AARRAR 9

DB 132 AARRAR 138

Search completed: August 9, 2003, 16:34:10

Job time : 21.4571 secs